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## SEQUENCE LISTING

<110> LEUNG, DAVID W.  
ADOUREL, DANIEL  
HOLLENBACK, DAVID

<120> MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE

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<140> 09/970,989  
<141> 2001-10-05

<150> 09/215,252  
<151> 1998-12-18

<150> 08/618,651  
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 Ala Val Leu Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu  
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 Asn Met Lys Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr  
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 100 105 110  
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 Thr Ser Thr Leu Val Ser Pro Lys Tyr Gly Val Phe Asn Arg Gly Cys  
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Gly Asn Ala Ile Tyr Ile Ala Asn His Gln Asn Asn Tyr Asp Met Val  
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Ser Ala Val Ser Ile Met Arg Asp Phe Val Pro Ala Ile Tyr Asp Thr  
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 Gly Arg Thr Val Glu Asn Met Ser Ile Ile Gly Trp Phe Val Arg Ser  
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 50 55 60  
 Trp Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val  
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 Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val Ser  
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 Ser Phe Tyr Asn Thr Lys Lys Phe Phe Thr Ser Gly Thr Val Thr  
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Ser Asn Val Gly Ile Val Ala Arg Trp Phe Gly Arg Leu Phe Thr Tyr  
 35 40 45

Pro Leu Phe Gly Leu Lys Val Glu His Arg Ile Pro Gln Asp Gln Lys  
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Gln Ile Ser Arg Ala Ile Tyr Ile Gly Asn His Gln Asn Asn Tyr Asp  
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Lys Lys Ser Leu Ile Trp Ile Pro Phe Phe Phe Thr Gly Ile Leu Tyr  
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Trp Val Thr Gly Asn Ile Phe Leu Asp Arg Glu Asn Arg Thr Lys Ala  
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His Asn Thr Met Ser Gln Leu Ala Arg Arg Ile Asn Glu Asp Asn Leu  
 130 135 140

Ser Ile Trp Met Phe Pro Glu Gly Thr Arg Asn Arg Gly Arg Gly Leu  
 145 150 155 160

Leu Pro Phe Lys Thr Gly Ala Phe Thr Phe His Ala Ala Ile Ser Ala  
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Gly Val Pro Ile Ile Pro Val Val Cys Ser Ser Thr His Asn Lys Ile  
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Asn Leu Asn Arg Trp Asp Asn Gly Lys Val Ile Cys Glu Ile Met Asp  
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His Ser Thr Ile Ala Ala Val Val Asn His Phe Lys Lys Arg Arg Ile  
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Gly Val Pro Ile Ile Pro Val Cys Val Ser Asn Thr Ser Asn Lys Val  
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 1 5 10 15

Pro Ala Val Ala Ala Thr Ala Asp Asp Asp Lys Asp Gly Val Phe Met  
 20 25 30

Val Leu Leu Ser Cys Phe Lys Ile Phe Val Cys Phe Ala Phe Thr Val  
 35 40 45

Val Leu Ile Thr Ala Val Ala Trp Gly Leu Ile Met Val Leu Leu Leu  
 50 55 60

Pro Trp Pro Tyr Met Arg Ile Arg Leu Gly Asn Leu Tyr Gly His Ile  
 65 70 75 80

Ile Gly Gly Leu Val Ile Trp Ile Tyr Gly Ile Pro Ile Lys Ile Gln  
 85 90 95

Gly Ser Glu His Thr Lys Lys Arg Ala Ile Phe Thr Tyr Ile Ser Asn  
 100 105 110

His Ala Ser Pro Ile Asp Ala Phe Phe Val Met Trp Leu Ala Pro Ile  
 115 120 125

Gly Thr Val Gly Val Ala Lys Lys Glu Val Ile Trp Tyr Pro Leu Leu  
 130 135 140

Gly Gln Leu Tyr Thr Leu Ala His His Ile Arg Ile Asp Arg Ser Asn  
 145 150 155 160

Pro Ala Ala Ala Ile Gln Ser Phe Thr Met Lys Glu Ala Val Arg Val  
 165 170 175

Ile Thr Glu Lys Asn Leu Ser Leu Ile Met Phe Pro Glu Gly Thr Arg  
 180 185 190

Ser Gly Asp Gly Arg Leu Leu Pro Phe Lys Lys Gly Phe Val His Leu  
 195 200 205

Ala Leu Gln Ser His Leu Pro Ile Val Pro Met Ile Leu Thr Gly Thr  
 210 215 220

His Leu Ala Trp Phe Thr Arg Lys Gly Thr Phe Arg Val Arg Pro Val  
 225 230 235 240

Pro Ile Thr Val Lys Tyr Leu Pro Pro Ile Asn Thr Asp Asp Trp Thr  
 245 250 255

Val Asp Lys Ile Asp Asp Tyr Val Lys Met Ile His Asp Ile Tyr Val  
 260 265 270

Arg Asn Leu Pro Ala Ser Gln Lys Pro Leu Gly Ser Thr Asn Arg Ser  
 275 280 285

Lys

<210> 11  
 <211> 318  
 <212> PRT  
 <213> Cocos nucifera

<400> 11  
 Met Asp Ala Ser Gly Ala Ser Ser Phe Leu Arg Gly Arg Cys Leu Glu  
 1 5 10 15

Ser Cys Phe Lys Ala Ser Phe Gly Met Ser Gln Pro Lys Asp Ala Ala  
 20 25 30

Gly Gln Pro Ser Arg Arg Pro Ala Asp Ala Asp Asp Phe Phe Thr Val  
 35 40 45

Asp Asp Asp Arg Trp Ile Thr Val Ile Leu Ser Val Val Arg Ile Ala  
 50 55 60

Ala Cys Phe Leu Ser Met Met Val Thr Thr Ile Val Trp Asn Met Ile  
 65 70 75 80

Met Leu Ile Leu Leu Pro Trp Pro Tyr Ala Arg Ile Arg Gln Gly Asn  
 85 90 95

Leu Tyr Gly His Val Thr Gly Arg Met Leu Phe Thr Met Trp Ile Leu  
 100 105 110

Gly Asn Pro Ile Thr Ile Glu Gly Ser Glu Phe Ser Asn Thr Arg Ala  
 115 120 125

Ile Tyr Ile Cys Asn His Ala Ser Leu Val Asp Ile Phe Leu Ile Met  
 130 135 140

Trp Leu Ile Pro Lys Gly Thr Val Thr Ile Ala Lys Lys Glu Ile Ile  
 145 150 155 160

Trp Tyr Pro Leu Phe Gly Gln Phe Thr Leu Tyr Val Leu Ala Asn His  
 165 170 175

Gln Arg Ile Asp Arg Ser Asn Pro Ser Ala Ala Ile Glu Ser Ile Lys  
 180 185 190

Glu Val Ala Arg Ala Val Val Lys Lys Asn Leu Ser Leu Ile Ile Phe  
 195 200 205

Pro Glu Gly Thr Arg Ser Lys Thr Gly Arg Leu Leu Pro Phe Lys Lys  
 210 215 220

Gly Phe Ile His Phe Thr Ile Ala Leu Gln Thr Arg Leu Pro Ile Val  
 225 230 235 240

Pro Met Val Leu Thr Gly Thr His Leu Ala Trp Arg Lys Asn Ser Leu  
 245 250 255

Arg Val Arg Pro Ala Pro Ile Thr Val Lys Tyr Phe Ser Pro Ile Lys  
 260 265 270

Thr Asp Asp Trp Glu Glu Lys Ile Asn His Tyr Val Glu Met Ile  
 275 280 285

His Phe Thr Ala Leu Tyr Val Asp His Leu Pro Glu Ser Gln Lys Pro  
 290 295 300

Leu Val Ser Lys Gly Arg Asp Ala Ser Gly Arg Ser Asn Ser  
 305 310 315

<210> 12

<211> 1660

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (184)..(1311)

<400> 12

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ggcaggtgtc tggcttgcc acccggaaagc cctgagggca gctgttccca ctggctctgc 120

tgacccttgc ctttggacgg ctgtcctcag cgagggggccg tgcacccgct cctgagcagc 180

gcc atg ggc ctg ctg gcc ttc ctg aag acc cag ttc gtg ctg cac ctg 228  
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu  
 1 5 10 15

ctg gtc ggc ttt gtc ttc gtg gtg agt ggt ctg gtc atc aac ttc gtc 276  
 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val  
 20 25 30

cag ctg tgc acg ctg gcg ctc tgg ccg gtc agc aag cag ctc tac cgc 324  
 Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg  
 35 40 45

cgc ctc aac tgc cgc ctc gca tac tca ctc tgg agc caa ctg gtc atg 372  
 Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met  
 50 55 60

ctg ctg gag tgg tgg tcc tgc acg gag tgt aca ctg ttc acg gac cag 420  
 Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln  
 65 70 75

gcc acg gta gag cgc ttt ggg aag gag cac gca gtc atc atc ctc aac 468  
 Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu Asn  
 80 85 90 95

cac aac ttc gag atc gac ttc ctc tgt ggg tgg acc atg tgt gag cgc	516
His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg	
100	105
110	
ttc gga gtg ctg ggg agc tcc aag gtc ctc gct aag aag gag ctg ctc	564
Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu	
115	120
125	
tac gtg ccc ctc atc ggc tgg acg tgg tac ttt ctg gag att gtg ttc	612
Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe	
130	135
140	
tgc aag cgg aag tgg gag gag gac cgg gac acc gtg gtc gaa ggg ctg	660
Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu	
145	150
155	
agg cgc ctg tcg gac tac ccc gag tac atg tgg ttt ctc ctg tac tgc	708
Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys	
160	165
170	175
gag ggg acg cgc ttc acg gag acc aag cac cgc gtt agc atg gag gtg	756
Glu Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val	
180	185
190	
gcg gct gct aag ggg ctt cct gtc ctc aag tac cac ctg ctg ccg cgg	804
Ala Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg	
195	200
205	
acc aag ggc ttc acc acc gca gtc aag tgc ctc cgg ggg aca gtc gca	852
Thr Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala	
210	215
220	
gct gtc tat gat gta acc ctg aac ttc aga gga aac aag aac ccg tcc	900
Ala Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser	
225	230
235	
ctg ctg ggg atc ctc tac ggg aag aag tac gag gcg gac atg tgc gtg	948
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val	
240	245
250	255
agg aga ttt cct ctg gaa gac atc ccc ctg gat gaa aag gaa gca gct	996
Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala	
260	265
270	
cag tgg ctt cat aaa ctg tac cag gag aag gac gcg ctc cag gag ata	1044
Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile	
275	280
285	
tat aat cag aag ggc atg ttt cca ggg gag cag ttt aag cct gcc cgg	1092
Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg	
290	295
300	
agg ccg tgg acc ctc ctg aac ttc ctg tcc tgg gcc acc att ctc ctg	1140
Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
305	310
315	

tct ccc ctc ttc agt ttt gtc ttg ggc gtc ttt gcc agc gga tca cct	1188
Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro	
320 325 330 335	
ctc ctg atc ctg act ttc ttg ggg ttt gtg gga gca gct tcc ttt gga	1236
Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly	
340 345 350	
gtt cgc aga ctg ata gga gta act gag ata gaa aaa ggc tcc agc tac	1284
Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr	
355 360 365	
gga aac caa gag ttt aag aaa aag gaa taattatgg ctgtgactga	1331
Gly Asn Gln Glu Phe Lys Lys Glu	
370 375	
acacacgcgg ccctgacggt ggtatccagt taactcaaaa ccaacacaca gagtgcagga	1391
aaagacaatt agaaaactatt tttcttatta actggtgact aatattaaca aaacttgagc	1451
caagagtaaa gaattcagaa ggccgtcag gtgaagtctt cagcctccca cagcgcaggg	1511
tcccagcatac tccacgcgcg cccgtggag gtgggtccgg ccggagagggc ctcccgccga	1571
cgccgtctct ccagaactcc gcttccaaga gggacctttg gctgctttct ctccctaaac	1631
tttagatcaaa ttttaaaaaaa aaaaaaaaaa	1660

<210> 13  
 <211> 376  
 <212> PRT  
 <213> Homo sapiens

<400> 13	
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu	
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Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln	
20 25 30	
Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg	
35 40 45	
Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu	
50 55 60	
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala	
65 70 75 80	
Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu Asn His	
85 90 95	
Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe	
100 105 110	
Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr	
115 120 125	

Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys  
 130 135 140  
 Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg  
 145 150 155 160  
 Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu  
 165 170 175  
 Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala  
 180 185 190  
 Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr  
 195 200 205  
 Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala  
 210 215 220  
 Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu  
 225 230 235 240  
 Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg  
 245 250 255  
 Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln  
 260 265 270  
 Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr  
 275 280 285  
 Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg  
 290 295 300  
 Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser  
 305 310 315 320  
 Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu  
 325 330 335  
 Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val  
 340 345 350  
 Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly  
 355 360 365  
 Asn Gln Glu Phe Lys Lys Lys Glu  
 370 375

<210> 14  
 <211> 1523  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (233)..(1174)

<400> 14  
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 ctactcaactc tggagcctag cacaaaacta gaagcaaccc aagcacctgt cactggagac 120  
 taattatgcg gcacccatac agggaccctc tgcggccatc atggagagcc ttcatcttgc 180  
 ccgtacagtt ttaagcgaaa aaggaagtat acaacaaagt ccataactgg tc atg ctg 238  
 Met Leu  
 1

ctg gag tgg tgg tcc tgc acg gag tgt aca ctg ttc acg gac cag gcc 286  
 Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala  
 5 10 15

acg gta gag cgc ttt ggg aag gag cac gca gtc atc atc ctc aac cac 334  
 Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu Asn His  
 20 25 30

aac ttc gag atc gac ttc ctc tgt ggg tgg acc atg tgt gag cgc ttc 382  
 Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe  
 35 40 45 50

gga gtg ctg ggg aag gtc ctc gct aag aag gag ctg ctc tac 430  
 Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr  
 55 60 65

gtg ccc ctc atc ggc tgg acg tgg tac ttt ctg gag att gtg ttc tgc 478  
 Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys  
 70 75 80

aag cgg aag tgg gag gag gac cgg gac acc gtg gtc gaa ggg ctg agg 526  
 Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg  
 85 90 95

cgc ctg tcg gac tac ccc gag tac atg tgg ttt ctc ctg tac tgc gag 574  
 Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu  
 100 105 110

ggg acg cgc ttc acg gag acc aag cac cgc gtt agc atg gag gtg gcg 622  
 Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala  
 115 120 125 130

gct gct aag ggg ctt cct gtc ctc aag tac cac ctg ctg ccg cgg acc 670  
 Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr  
 135 140 145

aag ggc ttc acc acc gca gtc aag tgc ctc cgg ggg aca gtc gca gct 718  
 Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala  
 150 155 160

gtc tat gat gta acc ctg aac ttc aga gga aac aag aac ccg tcc ctg 766  
 Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu  
 165 170 175

ctg ggg atc ctc tac ggg aag aag tac gag gcg gac atg tgc gtg agg	814
Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg	
180 185 190	
aga ttt cct ctg gaa gac atc ccg ctg gat gaa aag gaa gca gct cag	862
Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln	
195 200 205 210	
tgg ctt cat aaa ctg tac cag gag aag gac gcg ctc cag gag ata tat	910
Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr	
215 220 225	
aat cag aag ggc atg ttt cca ggg gag cag ttt aag cct gcc cgg agg	958
Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg	
230 235 240	
ccg tgg acc ctc ctg aac ttc ctg tcc tgg gcc acc att ctc ctg tct	1006
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser	
245 250 255	
ccc ctc ttc agt ttt gtc ttg ggc gtc ttt gcc agc gga tca cct ctc	1054
Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu	
260 265 270	
ctg atc ctg act ttc ttg ggg ttt gtg gga gca gct tcc ttt gga gtt	1102
Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val	
275 280 285 290	
cgc aga ctg ata gga gta act gag ata gaa aaa ggc tcc agc tac gga	1150
Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly	
295 300 305	
aac caa gag ttt aag aaa aag gaa taattatgg ctgtgactga acacacgcgg	1204
Asn Gln Glu Phe Lys Lys Lys Glu	
310	
ccctgacgggt ggtatccagt taactcaaaa ccaacacaca gagtgccagga aaagacaatt	1264
agaaaactatt tttcttattta actggtgact aatattaaca aaacttgagc caagagtaaa	1324
gaattcagaa ggcctgtcag gtgaagtctt cagcctccca cagcgcaggg tcccgacatc	1384
tccacgcgcg cccgtggag gtgggtccgg ccggagagggc ctccgcggc cgccgtctct	1444
ccagaactcc gttccaaga gggacctttg gctgcttct ctccttaaac ttagatcaaa	1504
ttttaaaaaaaa aaaaaaaaaa	1523

<210> 15  
 <211> 314  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp  
 1 5 10 15

Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu  
 20 25 30

Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu  
 35 40 45

Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu  
 50 55 60

Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val  
 65 70 75 80

Phe Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly  
 85 90 95

Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr  
 100 105 110

Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu  
 115 120 125

Val Ala Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro  
 130 135 140

Arg Thr Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val  
 145 150 155 160

Ala Ala Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro  
 165 170 175

Ser Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys  
 180 185 190

Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala  
 195 200 205

Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu  
 210 215 220

Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala  
 225 230 235 240

Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu  
 245 250 255

Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser  
 260 265 270

Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe  
 275 280 285

Gly Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser  
 290 295 300

Tyr Gly Asn Gln Glu Phe Lys Lys Glu  
 305 310

<210> 16  
 <211> 1774  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (158)..(1291)  
  
 <400> 16  
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 ggaaggagac gccttcctga gtcctggatc ttcttcctt ctggaaatct ttgactgtgg 120  
 gtagttatcc atttctgaat aagagcgtcc acgcattc atg gac ctc gcg gga ctg 175  
 Met Asp Leu Ala Gly Leu  
 1 5  
  
 ctg aag tct cag ttc ctg tgc caa ctg gtc ttc tgc tac gtc ttt att 223  
 Leu Lys Ser Gln Phe Leu Cys His Leu Val Phe Cys Tyr Val Phe Ile  
 10 15 20  
  
 gcc tca ggg cta atc atc aac acc att cag ctc ttc act ctc ctc ctc 271  
 Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln Leu Phe Thr Leu Leu Leu  
 25 30 35  
  
 tgg ccc att aac aag cag ctc ttc cgg aag atc aac tgc aga ctg tcc 319  
 Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys Ile Asn Cys Arg Leu Ser  
 40 45 50  
  
 tat tgc atc tca agc cag ctg gtg atg ctg ctg gag tgg tgg tgc ggc 367  
 Tyr Cys Ile Ser Ser Gln Leu Val Met Leu Leu Glu Trp Trp Ser Gly  
 55 60 65 70  
  
 acg gaa tgc acc atc ttc acg gac ccg cgc gcc tac ctc aag tat ggg 415  
 Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala Tyr Leu Lys Tyr Gly  
 75 80 85  
  
 aag gaa aat gcc atc gtg gtt ctc aac cac aag ttt gaa att gac ttt 463  
 Lys Glu Asn Ala Ile Val Val Leu Asn His Lys Phe Glu Ile Asp Phe  
 90 95 100  
  
 ctg tgt ggc tgg agc ctg tcc gaa cgc ttt ggg ctg tta ggg ggc tcc 511  
 Leu Cys Gly Trp Ser Leu Ser Glu Arg Phe Gly Leu Leu Gly Gly Ser  
 105 110 115  
  
 aag gtc ctg gcc aag aaa gag ctg gcc tat gtc cca att atc ggc tgg 559  
 Lys Val Leu Ala Lys Lys Glu Leu Ala Tyr Val Pro Ile Ile Gly Trp  
 120 125 130  
  
 atg tgg tac ttc acc gag atg gtc ttc tgt tcg cgc aag tgg gag cag 607  
 Met Trp Tyr Phe Thr Glu Met Val Phe Cys Ser Arg Lys Trp Glu Gln  
 135 140 145 150  
  
 gat cgc aag acg gtt gcc acc agt ttg cag cac ctc cgg gac tac ccc 655  
 Asp Arg Lys Thr Val Ala Thr Ser Leu Gln His Leu Arg Asp Tyr Pro  
 155 160 165

gag aag tat ttt ttc ctg att cac tgt gag ggc aca cgg ttc acg gag	703
Glu Lys Tyr Phe Phe Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu	
170 175 180	
aag aag cat gag atc agc atg cag gtg gcc cgg gcc aag ggg ctg cct	751
Lys Lys His Glu Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro	
185 190 195	
cgc ctc aag cat cac ctg ttg cca cga acc aag ggc ttc gcc atc acc	799
Arg Leu Lys His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr	
200 205 210	
gtg agg agc ttg aga aat gta gtt tca gct gta tat gac tgt aca ctc	847
Val Arg Ser Leu Arg Asn Val Ser Ala Val Tyr Asp Cys Thr Leu	
215 220 225 230	
aat ttc aga aat aat gaa aat cca aca ctg ctg gga gtc cta aac gga	895
Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly	
235 240 245	
aag aaa tac cat gca gat ttg tat gtt agg agg atc cca ctg gaa gac	943
Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu Asp	
250 255 260	
atc cct gaa gac gat gac gag tgc tgc gcc tgg ctg cac aag ctc tac	991
Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys Leu Tyr	
265 270 275	
cag gag aag gat gcc ttt cag gag gag tac tac agg acg ggc acc ttc	1039
Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr Tyr Arg Thr Gly Thr Phe	
280 285 290	
cca gag acg ccc atg gtg ccc cgg cgg ccc tgg acc ctc gtg aac	1087
Pro Glu Thr Pro Met Val Pro Pro Arg Arg Pro Trp Thr Leu Val Asn	
295 300 305 310	
tgg ctg ttt tgg gcc tcg ctg gtg ctc tac cct ttc ttc cag ttc ctg	1135
Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr Pro Phe Phe Gln Phe Leu	
315 320 325	
gtc agc atg atc agg agc ggg tct tcc ctg acg ctg gcc agc ttc atc	1183
Val Ser Met Ile Arg Ser Gly Ser Ser Leu Thr Leu Ala Ser Phe Ile	
330 335 340	
ctc gtc ttc ttt gtg gcc tcc gtg gga gtt cga tgg atg att ggt gtg	1231
Leu Val Phe Phe Val Ala Ser Val Gly Val Arg Trp Met Ile Gly Val	
345 350 355	
acg gaa att gac aag ggc tct gcc tac ggc aac tct gac agc aag cag	1279
Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly Asn Ser Asp Ser Lys Gln	
360 365 370	
aaa ctg aat gac tgactcaggg aggtgtcacc atccgaaggg aaccttgggg	1331
Lys Leu Asn Asp	
375	
aactggtggc ctctgcataat cctccttagt gggacacggc gacaaaggct gggtgagccc	1391

ctgctggca cggcggaaat cacgacctct ccagccaggg agtctggctc caaggccgga 1451  
 tggggaggaa gatgtttgt aatcttttt tccccatgtg ctttagtggg ctttggttt 1511  
 cttttgtgc gagtggtgt gagaatggct gtgtggtgag tgtgaactt gttctgtgat 1571  
 catagaaaagg gtattttagg ctgcagggga gggcagggct ggggaccgaa ggggacaagt 1631  
 tcccccttca tcctttggtg ctgagtttc tgtaaccctt ggttgcaga gataaagtga 1691  
 aaagtgcattt aggtgagatg actaaattat gcctccaaga aaaaaaaatt aaagtgcattt 1751  
 tctgggtcaa aaaaaaaaaaaa aaa 1774

<210> 17  
 <211> 378  
 <212> PRT  
 <213> Homo sapiens

<400> 17  
 Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val  
 1 5 10 15  
 Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln  
 20 25 30  
 Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys  
 35 40 45  
 Ile Asn Cys Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu  
 50 55 60  
 Leu Glu Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg  
 65 70 75 80  
 Ala Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His  
 85 90 95  
 Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg Phe  
 100 105 110  
 Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu Ala Tyr  
 115 120 125  
 Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met Val Phe Cys  
 130 135 140  
 Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala Thr Ser Leu Gln  
 145 150 155 160  
 His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe Leu Ile His Cys Glu  
 165 170 175  
 Gly Thr Arg Phe Thr Glu Lys Lys His Glu Ile Ser Met Gln Val Ala  
 180 185 190

Arg Ala Lys Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr  
 195 200 205  
 Lys Gly Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala  
 210 215 220  
 Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu  
 225 230 235 240  
 Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val Arg  
 245 250 255  
 Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala  
 260 265 270  
 Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr  
 275 280 285  
 Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg  
 290 295 300  
 Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr  
 305 310 315 320  
 Pro Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu  
 325 330 335  
 Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly Val  
 340 345 350  
 Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly  
 355 360 365  
 Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp  
 370 375

<210> 18

<211> 52

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 18

Pro Phe Lys Lys Gly Ala Phe His Leu Ala Gln Gln Gly Lys Ile Pro  
 1 5 10 15

Ile Val Pro Val Val Val Ser Asn Thr Ser Thr Leu Val Ser Pro Lys  
 20 25 30

Tyr Gly Val Phe Asn Arg Gly Cys Met Ile Val Arg Ile Leu Lys Pro  
 35 40 45

Ile Ser Thr Glu  
 50

&lt;210&gt; 19

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

Pro Ser Asn Cys Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro  
1 5 10 15Ile Val Pro Ile Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys  
20 25 30Glu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro  
35 40 45

Val Pro Thr Glu

50

&lt;210&gt; 20

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

&lt;400&gt; 20

tgcaagatgg aaggcgcc 18

&lt;210&gt; 21

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

Gly Ala Phe His Leu Ala  
1 5

&lt;210&gt; 22

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Saccharomyces cerevisiae

&lt;400&gt; 22

Gln Gln Gly Lys Ile Pro Ile Val Pro Val Val Val Ser Asn Thr Ser  
1 5 10 15Thr Leu Val Ser Pro Lys Tyr Gly Val Phe Asn Arg Gly Cys Met Ile  
20 25 30Val Arg Ile Leu Lys Pro Ile Ser Thr Glu Asn Leu Thr Lys Asp Lys  
35 40 45

Ile Gly Glu Phe Ala Glu Lys Val Arg Asp Gln Met  
 50 55 60

<210> 23  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Val Arg Glu Asn Val Pro Ile Val Pro Val Val Tyr Ser Ser Phe Ser  
 1 5 10 15

Ser Phe Tyr Asn Thr Lys Lys Phe Phe Thr Ser Gly Thr Val Thr  
 20 25 30

Val Gln Val Leu Glu Ala Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp  
 35 40 45

Val Pro Ala Leu Arg Gly Thr Pro Ala Thr Gly Pro  
 50 55 60

<210> 24  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 24  
 cctcaaagtg tggatctatc 20

<210> 25  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 25  
 ggaagagtac accacgggga c 21

<210> 26  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 26  
gactctagcc taggcttttg c

21

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 27  
ctagttata atacgactca c

21

<210> 28  
<211> 23  
<212> PRT  
<213> Zea mays

<400> 28  
Gly Leu Gln Arg Leu Lys Asp Phe Pro Arg Pro Phe Trp Leu Ala Leu  
1 5 10 15  
Phe Val Glu Gly Thr Arg Phe  
20

<210> 29  
<211> 23  
<212> PRT  
<213> Homo sapiens

<400> 29  
Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu  
1 5 10 15  
Tyr Cys Glu Gly Thr Arg Phe  
20

<210> 30  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 30  
gactaccccg agtacatgtg gtttctc

27

<210> 31  
<211> 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 31

Asp Tyr Pro Glu Tyr Met Trp Phe Leu  
1 5

&lt;210&gt; 32

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

&lt;400&gt; 32

cacatgtccg cctcgtaactt cttc

24

&lt;210&gt; 33

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu  
1 5 10 15Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln  
20 25 30Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr  
35 40 45

&lt;210&gt; 34

&lt;211&gt; 46

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val  
1 5 10 15Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln  
20 25 30Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe  
35 40 45

&lt;210&gt; 35

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer  
  
<400> 35  
ggctctagat attaatagta atcaattac 29

<210> 36  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer  
  
<400> 36  
cctcacgcat gcaccatggt aatagc. 26

<210> 37  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer  
  
<400> 37  
ggtgcatgcg tgaggctccg gtgc 24

<210> 38  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer  
  
<400> 38  
gtagtttca cggtacctga aatggaag 28

<210> 39  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer  
  
<400> 39  
ggcccggtac catgggcctg ctggcattcc 30

<210> 40  
<211> 33

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 40  
taactcctcg agttattcct ttttcttaaa ctc 33

<210> 41  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 41  
atggtgtgtac caccatggac ctcgcgggac tgctg 35

<210> 42  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 42  
ggaggatatac tagaggccac cagttc 26

<210> 43  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
6X-His tag

<400> 43  
His His His His His His  
1 5

<210> 44  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 44  
cacatgtccg cctcgtactt cttc

24

<210> 45  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Primer

<400> 45  
gactctagcc taggcttttg c

21